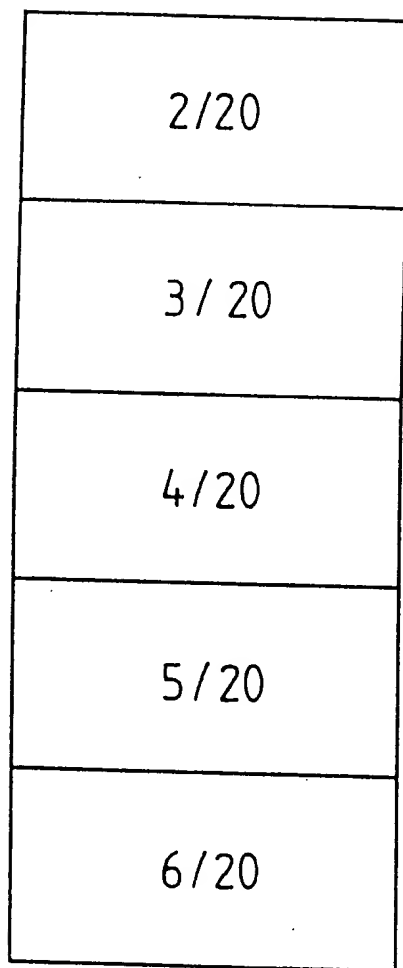


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4/20
5/20
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FIG 1

18

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FIG 1

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CCT AGA AAT CCA AAG GCT TGT ACC TTA AAC TGT GAT CCA AGA ATT GCC	306
Pro Arg Asn Pro Lys Ala Cys Thr Leu Asn Cys Asp Pro Arg Ile Ala	70
55 60 65	
TAT GGA GTT TGC CCG CGT TCA GAA AAG AAG AAT GAT CGG ATA TGC	354
Tyr Gly Val Cys Pro Arg Ser Glu Glu Lys Lys Asn Asp Arg Ile Cys	
75 80 85	
ACC AAC TGT TGC GCA GGC ACG AAG GGT TGT AAG TAC TTC AGT GAT GAT	402
Thr Asn Cys Cys Ala Gly Thr Lys Lys Gly Cys Lys Tyr Phe Ser Asp Asp	
90 95 100	
GGA ACT TTT GTT TGT GAA GGA GAG TCT GAT CCT AGA AAT CCA AAG GCT	450
Gly Thr Phe Val Cys Glu Gly Glu Ser Asp Pro Arg Asn Pro Lys Ala	
105 110 115	
TGT CCT CGG AAT TGC GAT CCA AGA ATT GCC TAT GGG ATT TGC CCA CTT	498
Cys Pro Arg Asn Cys Asp Pro Arg Ile Ala Tyr Gly Ile Cys Pro Leu	
120 125 130	
GCA GAA GAA AAG AAT GAT CGG ATA TGC ACC AAC TGT TGC GCA GGC	546
Ala Glu Glu Lys Lys Asn Asp Arg Ile Cys Thr Asn Cys Cys Ala Gly	
135 140 145 150	

FIG 1

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AAA AAG GGT TGT AAG TAC TTT AGT GAT GAT GGA ACT TTT GTT TGT GAA	594
Lys Lys Gly Cys 155	
	160
	165
	170
GGA GAG TCT GAT CCT AAA AAT CCA AAG GCC TGT CCT CGG AAT TGT GAT	642
Gly Glu Ser Asp Pro Lys Asn Pro Lys Ala Cys Pro	
	175
	180
	185
	190
	195
GGA AGA ATT GCC TAT GGG ATT TGC CCA CTT TCA GAA GAA AAG AAG AAT	690
Gly Arg Ile Ala Tyr Gly Ile Cys Pro Leu Ser Glu Glu Lys Lys Asn	
	200
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	895
	900
	905
	910
	915
	920
	925
	930
	935
	940
	945
	950
	955
	960
	965
	970
	975
	980
	985
	990
	995
	1000

FIG 1

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ATT TGC CCA CTT TCA GAA GAA AAG AAG AAT GAT CGG ATA TGC ACA AAC	882
Ile Cys Pro Leu Ser Glu Glu Lys Lys Asn Asp Arg Ile Cys Thr Asn	
250 255 260	
TGT TGC GCA GGC AAA AAG AAG GGC TGT AAG TAC TTT AGT GAT GAT GGA ACT	930
Cys Cys Ala Gly Lys Lys Gly Cys Lys Tyr Phe Ser Asp Asp Gly Thr	
265 270 275	
TTT GTT TGT GAA GAG GAG TCT GAT CCT AGA AAT CCA AAG GCC TGT CCT	978
Phe Val Cys Glu Gly Glu Ser Asp Pro Arg Asn Pro Lys Ala Cys Pro	
280 285 290	
CGG AAT TGT GAT GGA AGA ATT GCC TAT GGA ATT TGC CCA CTT TCA GAA	1026
Arg Asn Cys Asp Gly Arg Ile Ala Tyr Gly Ile Cys Pro Leu Ser Glu	
295 300 305 310	
GAA AAG AAG AAT GAT CGG ATA TGC ACC ACC AAT TGT TGC GCA GGC AAG AAG	1074
Glu Lys Lys Asn Asp Arg Ile Cys Thr Asn Cys Cys Ala Gly Lys Lys	
315 320 325	
GGC TGT AAG TAC TTT AGT GAT GAT GCA ACT TTT ATT TGT GAA GGA GAA	1122
Gly Cys Lys Tyr Phe Ser Asp Asp Gly Thr Phe Ile Cys Glu Gly Glu	
330 335 340	

FIG 1

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TCT GAA TAT GCC AGC AAA GTG GAT GAA TAT GTT GGT GAA GTG GAG AAT      1170
Ser Glu Tyr Ala Ser Lys Val Asp Glu Tyr Val Gly Glu Val Glu Asn
345                               350      355

GAT CTC CAG AAG TCT AAG GTT GCT GTT TCC TAAGTCCTAA CTAATAATAT      1220
Asp Leu Gln Lys Ser Lys Val Ala Val Ser
360                               365

GTAGTCTATG TATGAACAA AGCATGCCA ATATGCTCTG TCTTGCCTGT AATCTGTAAT      1280

ATGGTAGTGG AGCTTTTCCA CTGCCCTGTTT AATAAGAAAT GGAGCACTAG TTTGTTTTAG      1340

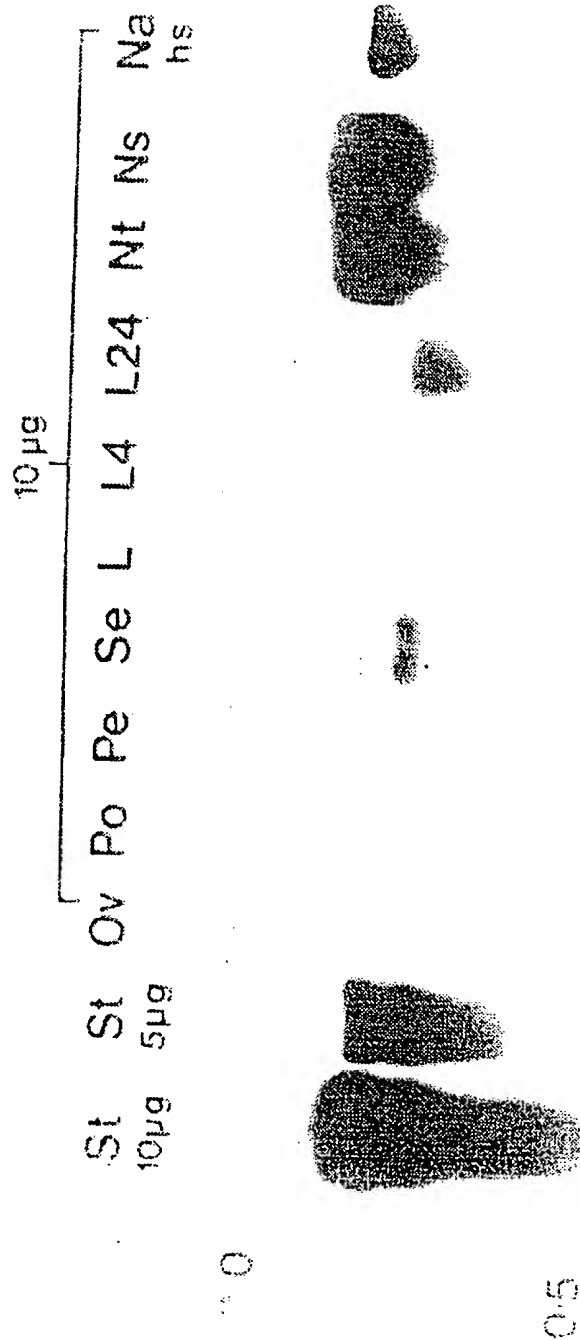
TTAAAAAAAAA AAAAAAAAAAA      1360

```

FIG 1

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FIG 2



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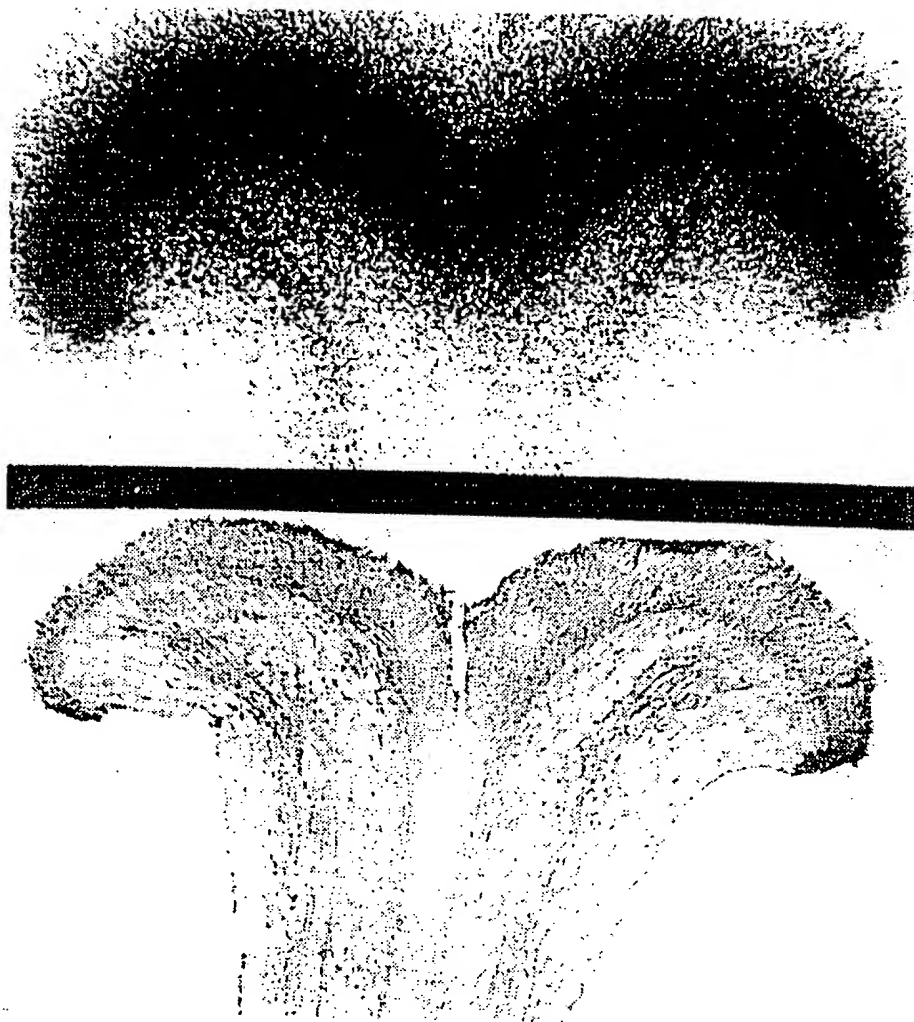


FIG 3

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EcoRI HindIII

9.4

6.5

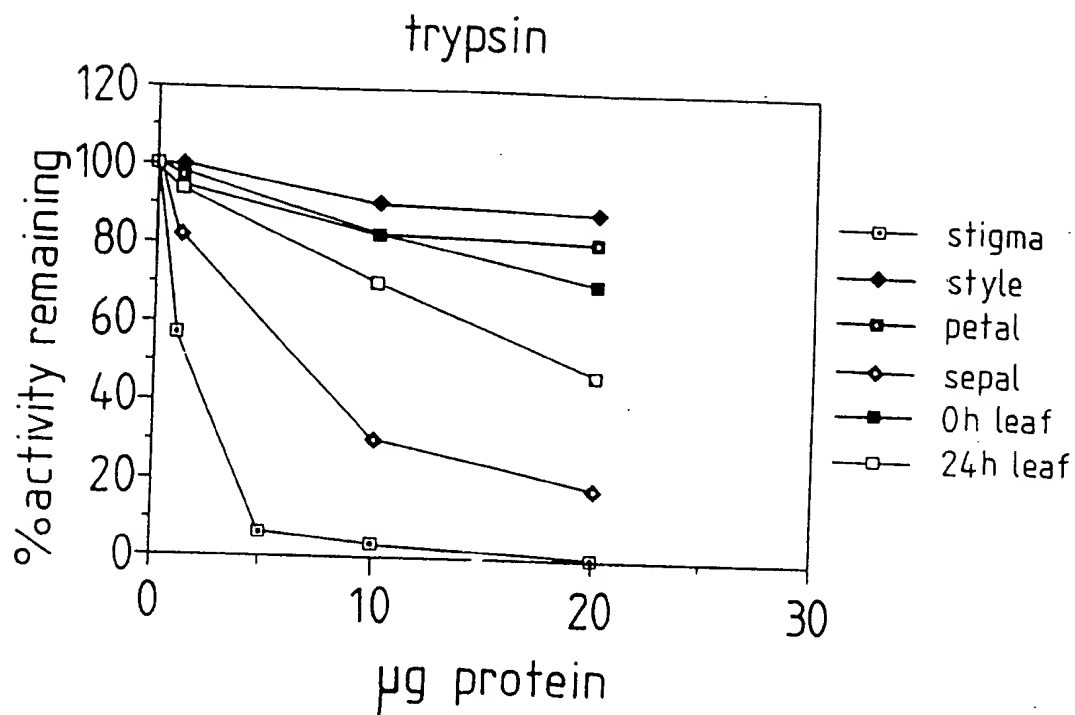
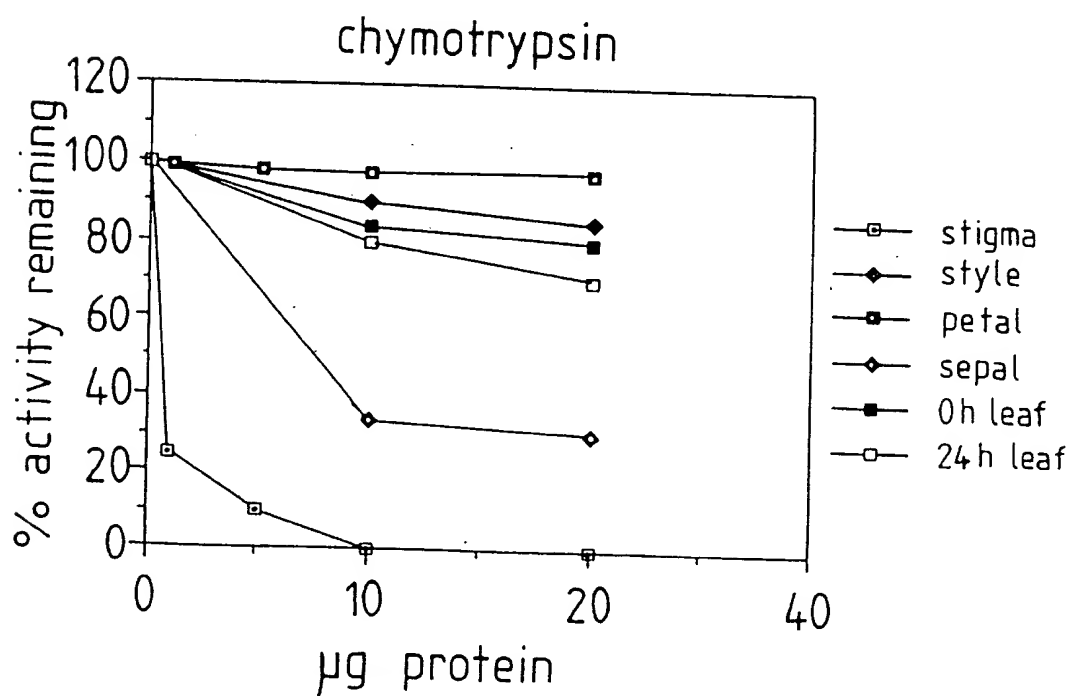
4.3

2.3

2.0

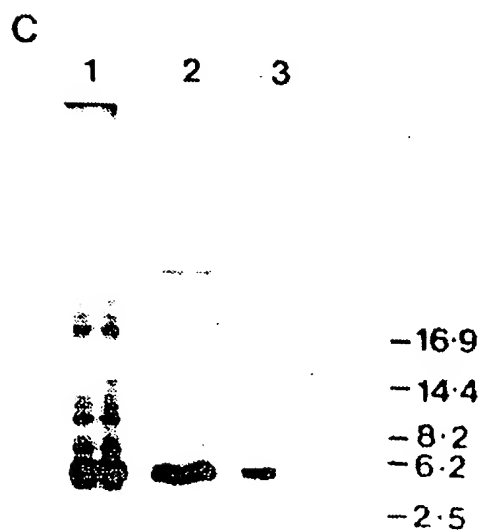
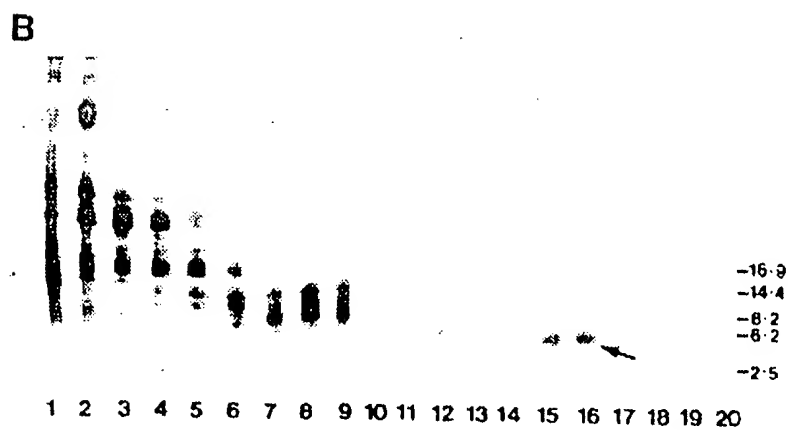
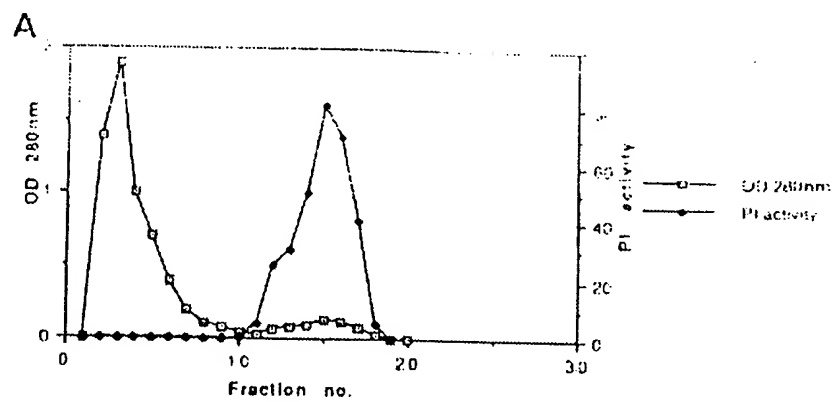
FIG 4

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FIGURE 5AFIGURE 5B

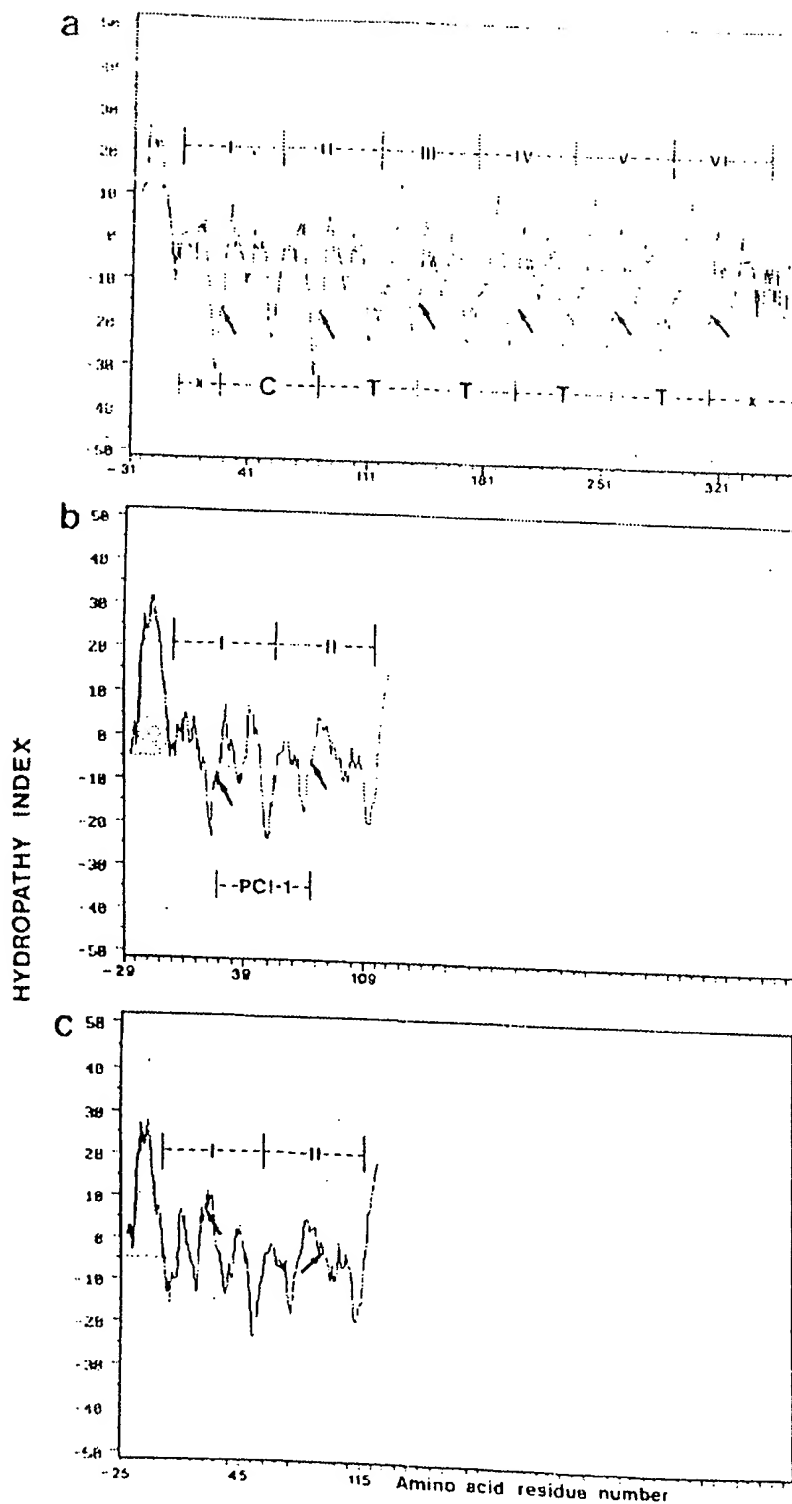
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FIG 6



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FIG 7



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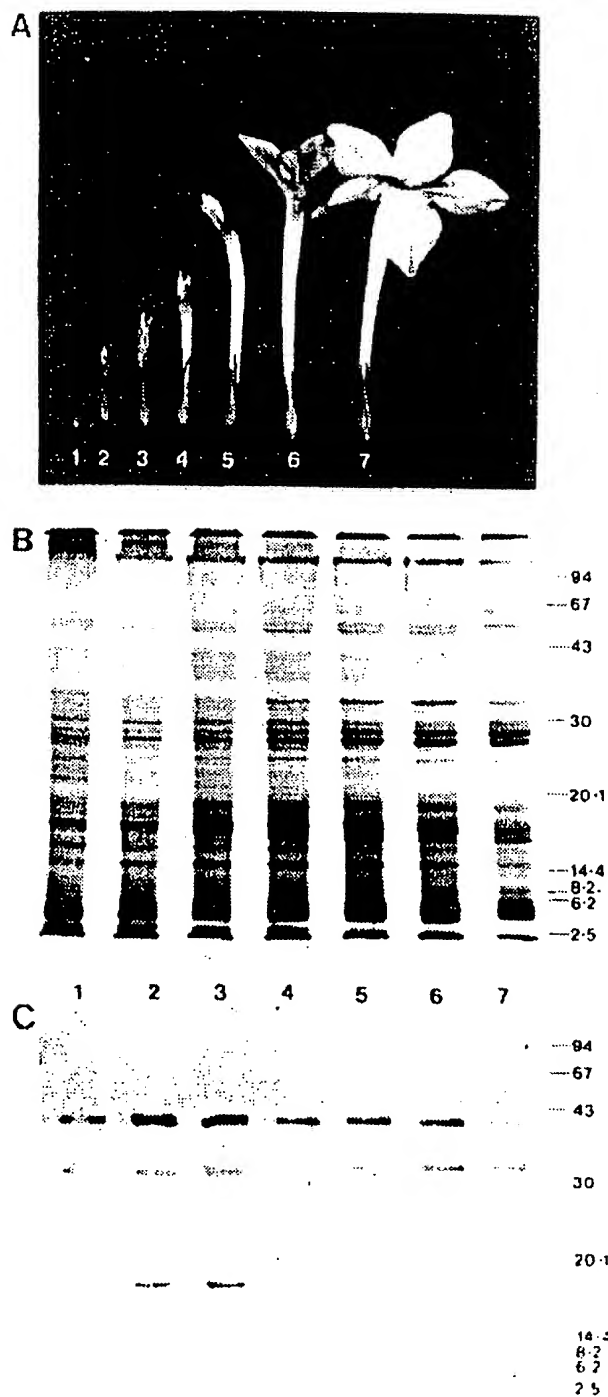


FIG 8

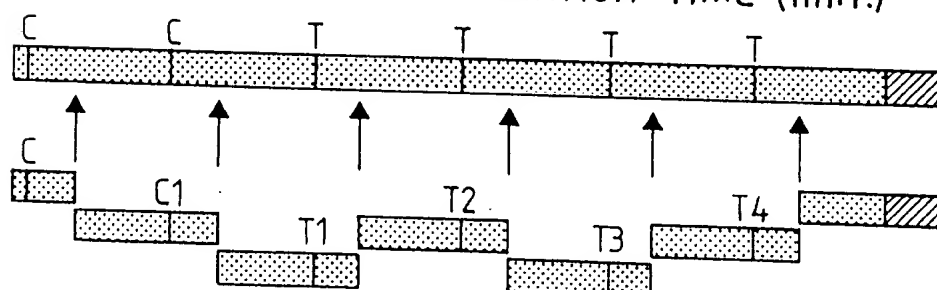
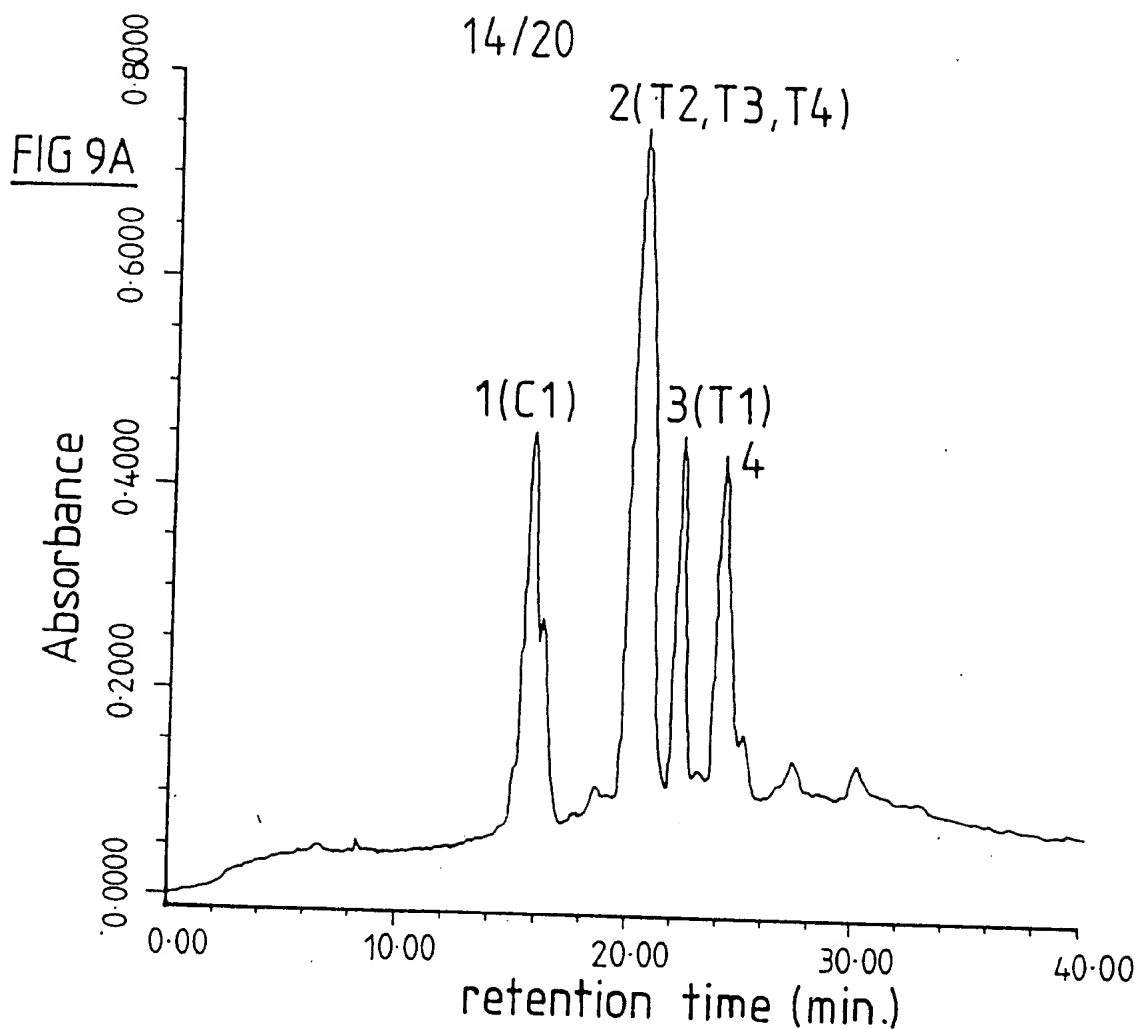


FIG 9B

C1 DRICTNCCAGTKGCKYFSDDGTFVCEGESDPRNPKACTLNCDPRIAYGVCPRS

T1 DRICTNCCAGTKGCKYFSDDGTFVCEGESDPRNPKACPRNCDPRIAYGICPL

T2 DRICTNCCAGKKGCKYFSDDGTFVCEGESDPKNPKACPRNCDGRIAYGICPLS

T3 DRICTNCCAGKKGCKYFSDDGTFVCEGESDPKNPKACPRNCDGRIAYGICPLS

T4 DRICTNCCAGKKGCKYFSDDGTFVCEGESDPRNPKACPRNCDGRIAYGICPLS

1 10 20 30 40 50

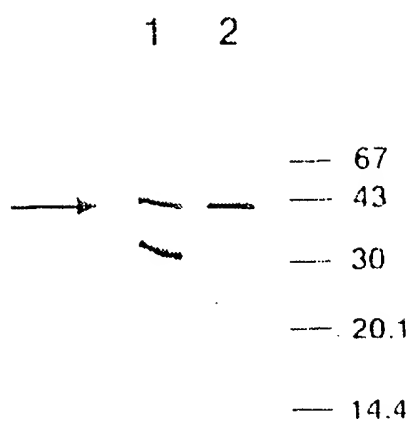
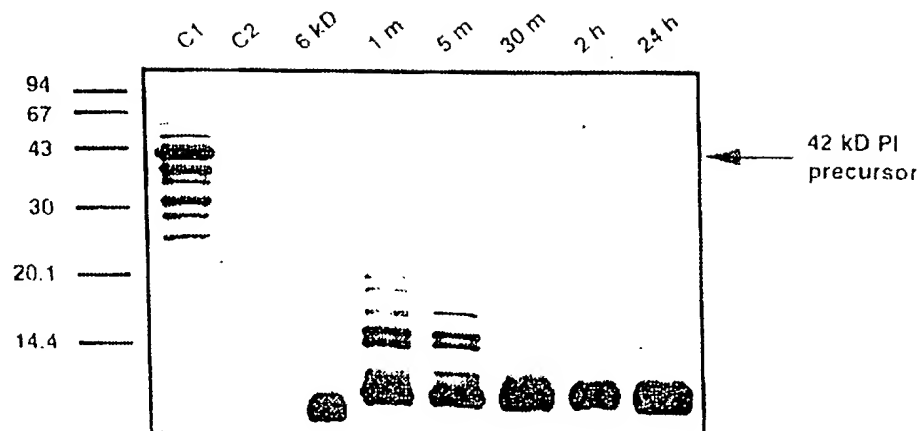
FIGURE 9C

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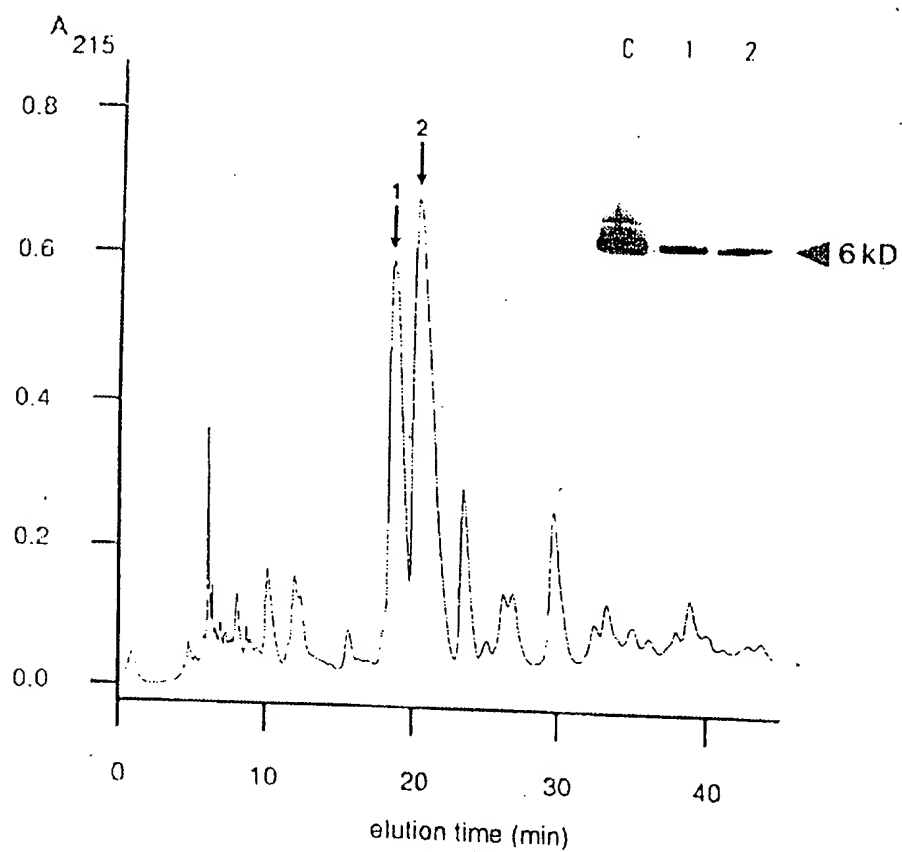
-10
1 10
ICP(R OF L)(S OF A)EEKKNDRICTNCCAG(T OF K)KG

FIGURE 10

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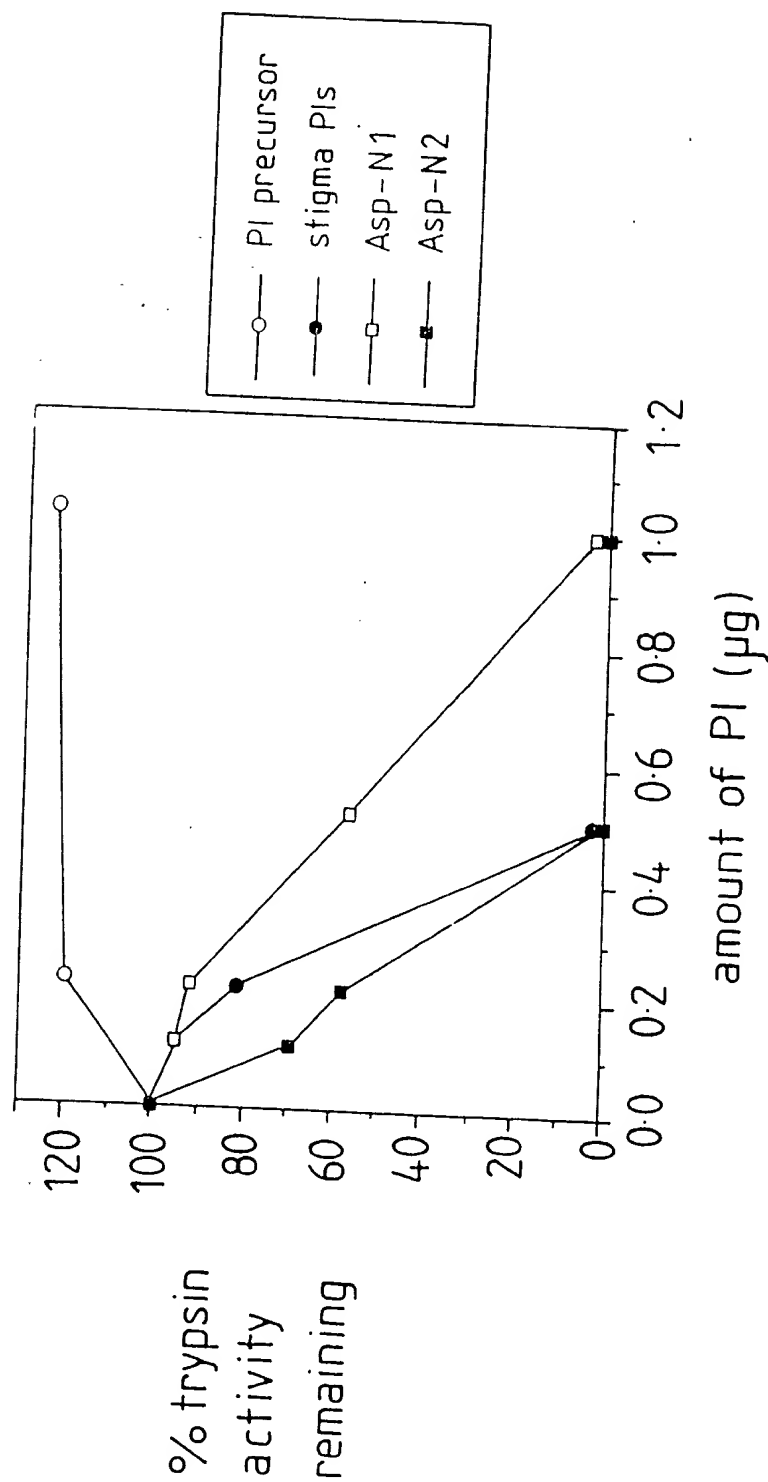
FIG 11AFIG 11B

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FIG 12

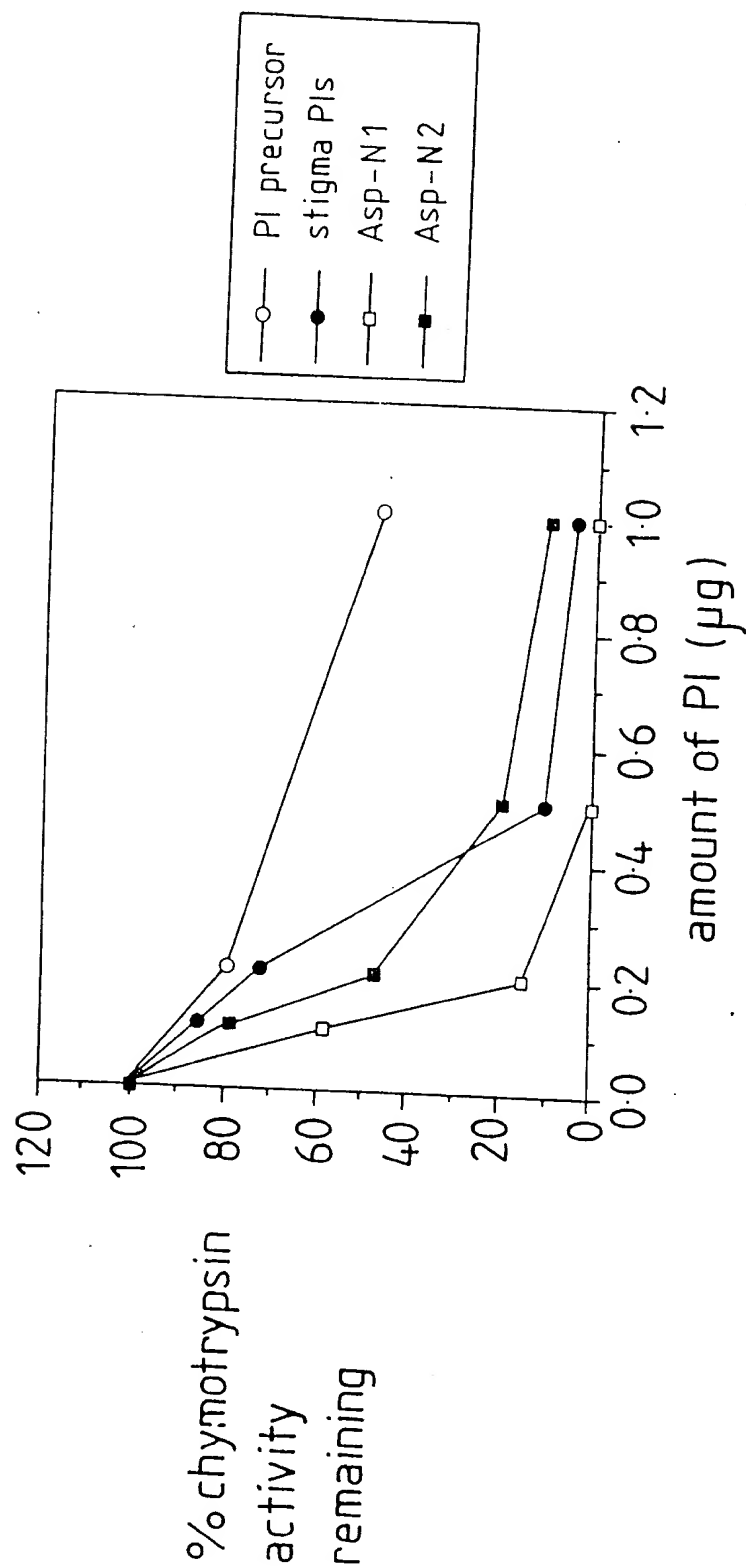
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FIGURE 13A

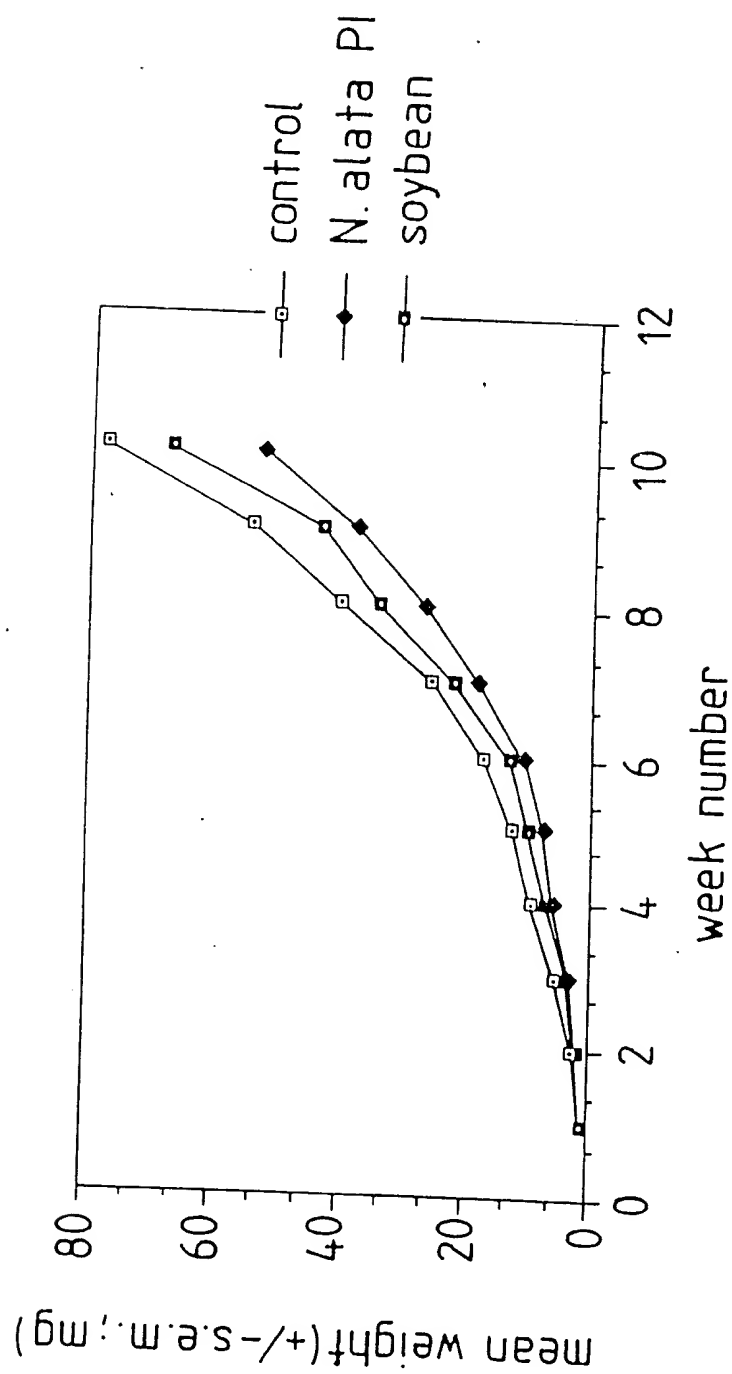


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FIGURE 13B



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FIGURE 14